

08/182,183
Part of #25

(1) GENERAL INFORMATION

- (i) APPLICANT: LIN, LEU-FEN
COLLINS, FRANKLIN D.
DOHERTY, DANIEL H.
LILE, JACK
BEKTESH, SUSAN
- (ii) TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: AMGEN INC.
(B) STREET: 1840 DeHavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy Disk
(B) COMPUTER: Macintosh
(C) OPERATING SYSTEM: 7.1
(D) SOFTWARE: Microsoft Word 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/182,183
(B) FILING DATE: 23-MAY-1994

(2) INFORMATION FOR SEQ ID NO:1

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (v) FRAGMENT TYPE: N-terminal fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Xaa
5 10 15

Gln Ala Ala Ala Ala Ser Pro Asp Asn
20 25

(2) INFORMATION FOR SEQ ID NO:2

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear
- (v) FRAGMENT TYPE: internal fragment
- (ix) FEATURE: Xaa is either Lys or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Xaa Ile Leu Lys Asn Leu Gly Arg Val Arg Arg Leu
5 10

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: nucleic acid for rat GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCCGGGCT GCAGGAATTC GGGG GTC TAC GGA GAC CGG ATC CGA GGT	48
Val Tyr Gly Asp Arg Ile Arg Gly	
-90	
GCC GCC GCC GGA CGG GAC TCT AAG ATG AAG TTA TGG GAT GTC GTG	93
Ala Ala Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val	
-85 -80 -75	
GCT GTC TGC CTG GTG TTG CTG CAC ACC GCG TCT GCC TTC CCG CTG	138
Ala Val Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu	
-70 -65 -60	
CCC GCC GGT AAG AGG CTT CTC GAA GCG CCC GCC GAA GAC CAC TCC	183
Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser	
-55 -50 -45	
CTC GGC CAC CGC CGC GTG CCC TTC GCG CTG ACC AGT GAC TCC AAT	228
Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr Ser Asp Ser Asn	
-40 -35 -30	
ATG CCC GAA GAT TAT CCT GAC CAG TTT GAT GAC GTC ATG GAT TTT	273
Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe	
-25 -20 -15	
ATT CAA GCC ACC ATC AAA AGA CTG AAA AGG TCA CCA GAT AAA CAA	318
Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln	
-10 -5 1 5	
GCG GCG GCA CTT CCT CGA AGA GAG AGG AAC CGG CAA GCT GCA GCT	363
Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala	
10 15 20	
GCC AGC CCA GAG AAT TCC AGA GGG AAA GGT CGC AGA GGC CAG AGG	408
Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg	
25 30 35	

GGC AAA AAT CGG GGG TGC GTC TTA ACT GCA ATA CAC TTA AAT GTC	453
Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val	
40 45 50	
ACT GAC TTG GGT TTG GGC TAC GAA ACC AAG GAG GAA CTG ATC TTT	498
Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe	
55 60 65	
CGA TAT TGT AGC GGT TCC TGT GAA GCG GCC GAG ACA ATG TAC GAC	543
Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp	
70 75 80	
AAA ATA CTA AAA AAT CTG TCT CGA AGT AGA AGG CTA ACA AGT GAC	588
Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp	
85 90 95	
AAG GTA GGC CAG GCA TGT TGC AGG CCG GTC GCC TTC GAC GAC GAC	633
Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp	
100 105 110	
CTG TCG TTT TTA GAC GAC AGC CTG GTT TAC CAT ATC CTA AGA AAG	678
Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys	
115 120 125	
CAT TCC GCT AAA CGG TGT GGA TGT ATC TGA CCCTGGCTCC	718
His Ser Ala Lys Arg Cys Gly Cys Ile	
130	
AGAGACTGCT GTGTATTGCA TTCCTGCTAC ACTGCGAAGA AAGGGACCAA	768
GGTTCCCAGG AAATATTTGC CCAGAAAGGA AGATAAGGAC CAAGAAGGCA	818
GAGGCAGAGG CGGAAGAAGA AGAAGAAAAG AAGGACGAAG GCAGCCATCT	868
GTGGGAGCCT GTAGAAGGAG GCCCAGCTAC AG	900

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: inferred amino acid sequence for mature rat GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
1 5 10 15
Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
20 25 30

Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

- (2) INFORMATION FOR SEQ ID NO:5
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 562 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: nucleic acid sequence for human GDNF
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTT TCTCTTTTCT TTTTGAACAG CA AAT ATG CCA GAG GAT TAT CCT	47
Ser Asn Met Pro Glu Asp Tyr Pro	
-25 -20	
GAT CAG TTC GAT GAT GTC ATG GAT TTT ATT CAA GCC ACC ATT	89
Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile	
-15 -10	
AAA AGA CTG AAA AGG TCA CCA GAT AAA CAA ATG GCA GTG CTT	131
Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu	
-5 1 5	
CCT AGA AGA GAG CGG AAT CGG CAG GCT GCA GCT GCC AAC CCA	173
Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Asn Pro	
10 15 20	
GAG AAT TCC AGA GGA AAA GGT CGG AGA GGC CAG AGG GGC AAA	215
Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys	
25 30 35	

AAC	CGG	GGT	TGT	GTC	TTA	ACT	GCA	ATA	CAT	TTA	AAT	GTC	ACT	257
Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	
		40					45					50		

GAC	TTG	GGT	CTG	GGC	TAT	GAA	ACC	AAG	GAG	GAA	CTG	ATT	TTT	299
Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	
		55						60					65	

AGG	TAC	TGC	AGC	GGC	TCT	TGC	GAT	GCA	GCT	GAG	ACA	ACG	TAC	341
Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Asp	Ala	Ala	Glu	Thr	Thr	Tyr	
			70					75						

GAC	AAA	ATA	TTG	AAA	AAC	TTA	TCC	AGA	AAT	AGA	AGG	CTG	GTG	383
Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Asn	Arg	Arg	Leu	Val	
80					85					90				

ACT	GAC	AAA	GTA	GGG	CAG	GCA	TGT	TGC	AGA	CCC	ATC	GCC	TTT	425
Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Ile	Ala	Phe	
95						100					105			

GAT	GAT	GAC	CTG	TCG	TTT	TTA	GAT	GAT	AAC	CTG	GTT	TAC	CAT	467
Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr	His	
		110					115					120		

ATT	CTA	AGA	AAG	CAT	TCC	GCT	AAA	AGG	TGT	GGA	TGT	ATC	TGA	509
Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys	Ile		
			125				130							

CTCCGGCTCC	AGAGACTGCT	GTGTATTGCA	TTCCTGCTAC	AGTGCAAAGA	559
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AAG	562
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(2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: inferred amino acid sequence for mature human GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser	Pro	Asp	Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1				5					10					15	

Gln	Ala	Ala	Ala	Ala	Asn	Pro	Glu	Asn	Ser	Arg	Gly	Lys	Gly	Arg	Arg
			20					25					30		

Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	Leu
			35				40					45			

Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

- (2) INFORMATION FOR SEQ ID NO:7
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: oligonucleotide probe
 - (D) OTHER INFORMATION: N at positions 3, 15, and 18 is inosine
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCNGAYAARC ARGCGCNGC

20

- (2) INFORMATION FOR SEQ ID NO:8
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: nucleic acid sequence for human GDNF
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCTCTCCCC CACCTCCCGC CTGCCCCGCGC A GGT GCC GCC GCC GGA
 Gly Ala Ala Ala Gly
 -5 46
 CGG GAC TTT AAG ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC
 Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys
 1 5 10 88
 CTG GTG CTG CTC CAC ACC GCG TCC GCC TTC CCG CTG CCC GCC
 Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala
 15 20 130

GGT AAG AGG CCT CCC GAG GCG CCC GCC GAA GAC CGC TCC CTC 172
 Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu
 25 30 35

GGC CGC CGC CGC GCG CCC TTC GCG CTG AGC AGT GAC T 209
 Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp
 40 45 50

GTAAGAACCG TTCC 223

- (2) INFORMATION FOR SEQ ID NO:9
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (A) NAME/KEY: linker
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCGAATTCG GG 12

- (2) INFORMATION FOR SEQ ID NO:10
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acid residues
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Asp Lys Gln Ala Ala Ala
 5

- (2) INFORMATION FOR SEQ ID NO:11
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (A) NAME/KEY: nucleic acid sequence from pBluescript
 SK-76.1
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGAGGAACC GGCAAGCTGC WGMWGYMWGM CCW 33

- (2) INFORMATION FOR SEQ ID NO:12
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acid residues
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Arg Asn Arg Gln Ala Ala Ala Ala Ser Pro
5 10

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide DHD-26
- (D) OTHER INFORMATION: N at positions 9 and 12 are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ARRTTYTTNA RNATYTTRTC

20

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asp Lys Ile Leu Lys Asn Leu
5

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide primer PD1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GACGGGACTC TAAGATG

17

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE

- (A) NAME/KEY: oligonucleotide primer DHD23

(D) OTHER INFORMATION: N at positions 3, 6, and 18 is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCNGCNGCYT GYTTRTCNGG

20

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer LF2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGAGACAATG TACGACA

17

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer PD2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCTGGAGCC AGGGTCA

17

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer PD1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCCGAATTCG ACGGGACTCT AAGATG

26

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer LFA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGTGGCCAG AGGGAGTGGT CTTC

24

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer PD3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGGATCCA ATAAGGAGGA AAAAAAATGT CACCAGATAA ACAAAT

46

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide primer PD4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGCGGTACCC AGTCTCTGGA GCCGGA

26

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: adapter fragment for plasmid pCJ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCTAGAAT TGTCATGTTT GACAGCTTAT CAT

33

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: polylinker sequence for plasmid pCJX1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

AATTCCCGGG TACCAGATCT GAGCTCACTA GTCTGCA

37

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: nucleic acid sequence for human GDNF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

TTCTCTCCCC CACCTCCCGC CTGCCCCGCGC A GGT GCC GCC GCC GGA	46
Gly Ala Ala Ala Gly	
CGG GAC TTT AAG ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC	88
Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys	
CTG GTG CTG CTC CAC ACC GCG TCC GCC TTC CCG CTG CCC GCC	130
Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala	
GGT AAG AGG CCT CCC GAG GCG CCC GCC GAA GAC CGC TCC CTC	172
Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu	
GGC CGC CGC CGC GCG CCC TTC GCG CTG AGC AGT GAC TCA AAT	214
Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser Asn	
ATG CCA GAG GAT TAT CCT GAT CAG TTC GAT GAT GTC ATG GAT	256
Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp	
TTT ATT CAA GCC ACC ATT AAA AGA CTG AAA AGG TCA CCA GAT	298
Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp	
1	
AAA CAA ATG GCA GTG CTT CCT AGA AGA GAG CGG AAT CGG CAG	340
Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln	
5 10 15	
GCT GCA GCT GCC AAC CCA GAG AAT TCC AGA GGA AAA GGT CGG	382
Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg	
20 25 30	
AGA GGC CAG AGG GGC AAA AAC CGG GGT TGT GTC TTA ACT GCA	424
Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala	
35 40 45	
ATA CAT TTA AAT GTC ACT GAC TTG GGT CTG GGC TAT GAA ACC	466
Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr	
50 55	

AAG GAG GAA CTG ATT TTT AGG TAC TGC AGC GGC TCT TGC GAT	508
Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp	
60 65 70	
GCA GCT GAG ACA ACG TAC GAC AAA ATA TTG AAA AAC TTA TCC	550
Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser	
75 80 85	
AGA AAT AGA AGG CTG GTG ACT GAC AAA GTA GGG CAG GCA TGT	592
Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys	
90 95 100	
TGC AGA CCC ATC GCC TTT GAT GAT GAC CTG TCG TTT TTA GAT	634
Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp	
105 110 115	
GAT AAC CTG GTT TAC CAT ATT CTA AGA AAG CAT TCC GCT AAA	676
Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys	
120 125	
AGG TGT GGA TGT ATC TGA CTCCGGCTCC AGAGACTGCT GTGTATTGCA	724
Arg Cys Gly Cys Ile	
130	
TTCCTGCTAC AGTGCAAAGA AAG	747